NEW UNITED STATES UTILITY PATENT APPLICATION
under 37 C.F.R. 1.53(b)

 Atty. Docket No. 03037.86702

Assistant Commissioner of Patents
Box Patent Applications
Washington, D.C. 20231

Enclosed herewith is a new patent application and the following papers:

First Named Inventor (or application identifier): Lynn M. Adams

Title of Invention: ENHANCERS OF CFTR CHLORIDE CHANNEL FUNCTION

1. ■ Specification 25 pages (including specification, claims, abstract) / 35 claims (3 independent)

2. ■ Declaration/Power of Attorney is:
   - ☐ attached in the regular manner.
   - ■ NOT included, but deferred under 37 C.F.R. § 1.53(f).

3. ■ 4 Distinct sheets of ■ Formal ☐ Informal Drawings

4. ☐ Preliminary Amendment.

5. ☐ Information Disclosure Statement
   - ☐ Form 1449
   - ☐ A copy of each cited prior art reference

6. ☐ Assignment with Cover Sheet.

7. ■ Priority is hereby claimed under 35 U.S.C. § 119 based upon the following application(s):

Country	Application Number	Date of Filing (day, month, year)
U.S.	60/121,495	24 February 1999

8. ☐ Priority document(s).

9. ☐ Statement Claiming Small Entity Status.

10. ☐ Microfiche Computer Program (Appendix).

11. ■ Nucleotide and/or Amino Acid Sequence Submission.
   - ☐ Computer Readable Copy.
   - ■ Paper Copy (identical to computer copy).
   - ■ Statement verifying identity of above copies.

NEW UNITED STATES UTILITY PATENT APPLICATION

under 37 C.F.R. 1.53(b)

12. Calculation of Fees:

FEES FOR	EXCESS CLAIMS	FEE	AMOUNT DUE
Basic Filing Fee (37 C.F.R. § 1.16(a))			$690.00
Total Claims in Excess of 20 (37 C.F.R. § 1.16(c))	15	18.00	$270.00
Independent Claims in Excess of 3 (37 C.F.R. § 1.16(b))	0	78.00	$0.00
Multiple Dependent Claims (37 C.F.R. § 1.16(d))	1	260.00	$260.00
Subtotal - Filing Fee Due			$1,220.00
	REDUCE BY (%)	($)	
Reduction by 50%, if Small Entity (37 C.F.R. §§ 1.9, 1.27, 1.28)	0		$610.00
TOTAL FILING FEE DUE			$610.00
Assignment Recordation Fee (if applicable) (37 C.F.R. § 1.21(h))	0	40.00	$0.00
GRAND TOTAL DUE			**$610.00**

13. PAYMENT is:

☐ included in the amount of the GRAND TOTAL by our enclosed check. A general authorization under 37 C.F.R. § 1.25(b), second sentence, is hereby given to credit or debit our Deposit Account No. 19-0733 for the instant filing and for any other fees during the pendency of this application under 37 C.F.R. §§ 1.16, 1.17 and 1.18.

■ not included, but deferred under 37 C.F.R. § 1.53(f).

14. All correspondence for the attached application should be directed to:

Banner & Witcoff, Ltd.
1001 G Street, N.W.
Washington, D. C. 20001-4597
Telephone: (202) 508-9100
Facsimile: (202) 508-9299

15. Other: _____

Date: February 24, 2000

By: Lisa M. Hemmendinger
Lisa M. Hemmendinger
Reg. No. 42,653

LMH/ama

ENHANCERS OF CFTR CHLORIDE CHANNEL FUNCTION

This application claims the benefit of co-pending provisional application Serial No. 60/121,495, filed February 24, 1999, which is incorporated by reference herein.

This invention was made with government support under RO1 HL/DK 49003, P30 DK27651 and RO1 DK51770 awarded by the National Institute of Health. The government has certain rights in the invention.

TECHNICAL FIELD OF THE INVENTION

This invention is related to the field of cystic fibrosis. More particularly, it is related to the area of therapeutic treatments and drug discovery for treating cystic fibrosis.

BACKGROUND OF THE INVENTION

Defects in CFTR, a chloride channel located in the apical membrane of epithelial cells, are associated with the common genetic disease, cystic fibrosis (Quinton, 1986, Welsh and Smith, 1993, Zielenski and Tsui, 1995). CFTR is a 1480 amino acid protein that is a member of the ATP binding cassette (ABC) transporter family (Riordan et al., 1989, Higgins, 1992). Each half of CFTR contains a transmembrane domain and a nucleotide binding fold (NBF), and the two halves are connected by a regulatory, or R domain. The R domain is unique to CFTR and contains several consensus PKA phosphorylation sites (Cheng et al., 1991, Picciotto et al., 1992).

Opening of the CFTR channel is controlled by PKA phosphorylation of

serine residues in the R domain (Tabcharani et al., 1991, Bear et al., 1992) and ATP binding and hydrolysis at the NBFs (Anderson et al., 1991, Gunderson and Kopito, 1995). Phosphorylation adds negative charges to the R domain, and introduces global conformational changes reflected by the reduction in the α-helical content of the R domain protein (Dulhanty and Riordan, 1994). Thus, electrostatic and/or allosteric changes mediated by phosphorylation are likely to be responsible for interactions between the R domain and other CFTR domains that regulate channel function (Rich et al., 1993, Gadsby and Nairn, 1994).

Rich et al., 1991 showed that deletion of amino acids 708-835 from the R domain (ΔR-CFTR), which removes most of the PKA consensus sites, renders the CFTR channel PKA independent, but the open probability of ΔR-CFTR is one-third that of the wild type channel and does not increase upon PKA phosphorylation (Ma et al., 1997, Winter and Welsh, 1997). Thus, it is possible that deletion of the R domain removes both inhibitory and stimulatory effects conferred by the R domain on CFTR chloride channel function. This conclusion is supported by studies that show that addition of exogenous unphosphorylated R domain protein (amino acids 588-858) to wt-CFTR blocks the chloride channel (Ma et al., 1996), suggesting that the unphosphorylated R domain is inhibitory. Conversely, exogenous phosphorylated R domain protein (amino acids 588-855 or 645-834) stimulated the ΔR-CFTR channel, suggesting that the phosphorylated R domain is stimulatory (Ma et al., 1997, Winter and Welsh, 1997). Therefore, it appears that the manifest activity (stimulatory or inhibitory) depends on the phosphorylation state of the R domain.

About 25% of the known 700 mutations in CFTR produce a mutant CFTR

protein which is properly transported to the apical membrane of epithelial cells but have only low level, residual channel activity. There is a need in the art for agents which can boost the level of channel activity in those mutants having low level activity.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide an isolated polypeptide useful for enhancing the open probability of CFTR chloride channels.

It is another object of the present invention to provide a method of activating a CFTR protein to enhance its open probability.

These and other objects of the invention are achieved by providing one or more of the embodiments described below. In one embodiment of the invention an isolated polypeptide is provided. The polypeptide comprises a portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein of between 10 and 100 amino acids, said portion comprising 18 amino acids as shown in SEQ ID NO: 1.

In another embodiment of the invention a method is provided for activating a CFTR protein. A polypeptide is applied to a CFTR protein which forms a cAMP regulated chloride channel. The polypeptide consists of a portion of CFTR protein which comprises 18 amino acids as shown in SEQ ID NO: 1, whereby the open probability of the channel formed by the CFTR increases by at least 25%.

According to another aspect of the invention a method is provided for activating a CFTR protein. A polypeptide is applied to a CFTR protein which forms a cAMP regulated chloride channel. The polypeptide consists of a portion of CFTR protein which comprises 22 amino acids as shown in SEQ ID NO: 2, whereby the

open probability of the channel formed by the CFTR increases by at least 25%.

The present invention thus provides the art with reagents and tools for enhancing function of channels which are defective in cystic fibrosis patients.

DETAILED DESCRIPTION OF THE DRAWINGS

Figure 1. Deletion of Negatively Charged Regions from the R Domain Results in Expression of Mature Glycosylated, Phosphorylatable CFTR Proteins

(Figure 1A) Sequences of NEG1 and NEG2 within the R domain. Residues where mutations have been identified in the CFTR cDNA are underlined (E822K, E826K, D836Y).

(Figure 1B) NEG2 is predicted to form an amphipathic α-helix as determined by secondary structure determination (Geourjon and Deleage, 1995, Rost and Sander, 1993, Rost and Sander, 1994) and illustrated in this space filling model. Negatively charged residues are colored pink, and the positively charged lysine is colored green.

(Figure 1C) In vitro phosphorylation of wt-(lane 1), ΔNEG1- (lane 2) and ΔNEG2-CFTR (lane 3) by PKA in the presence of γ-^{32}P-ATP. Both the core (band B) and fully glycosylated (band C) forms of all three CFTR molecules are phosphorylated.

Figure 2. ΔNEG2-CFTR Forms a Chloride Channel that is Unregulated by PKA

(Figure 2A) Single channel currents of wt, ΔNEG1- and ΔNEG2-CFTR incorporated into the lipid bilayer. While activities of wt-and ΔNEG1-CFTR absolutely require the presence of PKA in the *cis*-intracellular solution, the ΔNEG2-CFTR channel opens without PKA phosphorylation.

(Figure 2B) Diary plot of ΔNEG2-CFTR channel open probability versus time shows

that addition of 200 units/ml of PKA, a maximally stimulating concentration, does not affect channel activity. The dashed line indicates the average open probability for each segment of the experiment. Channels were recorded at –100 mV.

Figure 3. The Synthetic NEG2 Peptide both Stimulates and Inhibits CFTR

(Figure 3A) Diary plot (open probability versus time) of a wt-CFTR channel illustrating the effect of the NEG2 peptide on the open probability of the channel in the planar lipid bilayer. The concentration of synthetic NEG2 in the *cis*-intracellular solution is indicated above the plot.

(Figure 3B) Single channel currents from the wt-CFTR channel were acquired at –80 mV at the points indicated in A. The *cis*-intracellular solution contained 2 mM ATP and 50 units PKA/ml.

(Figure 3C) Single channel trace from ΔNEG2-CFTR incorporated into the lipid bilayer membrane. Traces were acquired at –80 mV. The *cis*-solution contained 2 mM ATP and no PKA. The top two traces were acquired before synthetic NEG2 peptide addition, with the second trace being an expansion of the first. In the bottom two traces, 0.44 μM of the NEG2 peptide has been added and stimulation is observed. The closed time visibly decreases after peptide addition.

Figure 4. NEG2 Enhances CFTR Channel Activity by Increasing the Opening Rate of the Channel

Histograms of open and closed events of the wt-CFTR channel at –80 mV were generated without peptide (control, left panel) and with 4.4 μM NEG2 peptide in the *cis*-solution (right panel).

(Figure 4A) The open time histograms contain a single exponential component with a time constant of 124 ms (control) and 105 ms (peptide-stimulated).

(Figure 4B) The closed time histograms contain a fast component and multiple slow components.

(Figure 4C) The closed-burst duration histograms were constructed using a delimiter of 40 ms (represented by the arrow in B). The solid lines in C represent the fit according to the double exponential equation $y = P_2*\exp[t-\alpha - \exp\alpha t-\alpha)]_2 + P_3*\exp[t-\alpha_3-\exp(t-\alpha_3)]$ where $\alpha_2 = \log \tau_{c2}$ $\alpha_3 = \log \tau_{c3}$ P_2 = probability of the intermediate closed component, and P_3 = probability of the long closed component. The best fit parameters are $P_2 = 0.811$, $\tau_{c2} = 459$ ms, $P_3 = 0.189$, $\tau_{c3} = 2494$ ms (control); $P_2 = 0.957$, $\tau_{c2} = 105$ ms, $P_3 = 0.043$, $\tau_{c3} = 1652$ ms (peptide-stimulated).

DETAILED DESCRIPTION OF THE INVENTION

It is a discovery of the present inventors that negatively charged amino acids at the carboxyl terminal of the R domain (817-838, NEG2) is involved in both the stimulatory and inhibitory functions of the R domain on the chloride channel. Moreover, a polypeptide which contains this portion of the CFTR amino acid sequence can be used to enhance the open probability of both wild-type and minimally active mutant CFTR protein.

The isolated polypeptide according to the invention consists of a portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein. The portion preferably contains at least 18 amino acids as shown in SEQ ID NO: 1. However, fewer amino acid residues of the sequence may be used if they retain the channel enhancing function described herein for the 18 and 22 residue polypeptides. See also SEQ ID NO: 2. Thus the polypeptide may be from about 10 or 15 amino acid residues up to about 30 or even 100 amino acid residues. An isolated polypeptide may be synthetic or made in a

recombinant organism. It may be a proteolytic cleavage product of a larger primary expression product, including full-length, wild-type CFTR. Preferably the polypeptide will be free of full-length CFTR. The polypeptide will preferably be free of other proteins and polypeptides as well. However, it may be desirable that the polypeptide be fused to another polypeptide to provide additional functional properties. For example, fusion to another protein such as keyhole limpet hemocyanin would be used to increase immunogenicity. Another desirable fusion partner is a membrane-penetrating peptide. Such peptides include VP-22 (SEQ ID NO: 3), as well as the peptides shown in SEQ ID NO: 4 and SEQ ID NO: 5. Such peptides can be used to facilitate the uptake by target cells of the polypeptide.

The polypeptides of the present invention can be used to enhance the function of wild-type or minimally active mutant CFTR proteins. The polypeptide functions to decrease the closed time of the channels formed by CFTR. A polypeptide can be applied to the CFTR protein in any context. It can be applied *in vitro* or *in vivo*. If *in vitro* it can be to CFTR in cultured cells or to planar bilayer membranes containing CFTR. If *in vivo,* the polypeptide can be applied directly to airway epithelial cells. Such application can be by any means known in the art, including but not limited to using a gargle or a nebulizer to deliver aerosolized polypeptide to the target cells. In addition, the peptide can be delivered in an indirect mode, by delivering a gene construct to the airway epithelial cells, which when taken up by the cells causes them to express the polypeptide. The delivery of the polypeptide to the CFTR preferably increases the open probability of the channel formed by the CFTR by at least 25%. More preferably it increases the open probability by at least 50%, at least 75%, at least 100%, at least 125%, at least 150%, or at least 200%.

A CFTR construct comprises a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO: 1. A suitable promoter for expression in lung epithelia is also desirable. Many such promoters are known in the art, and any can be used as appropriate for a particular application.

It is believed that the administration of the polypeptide of the present invention will be the most useful in treatment of a class of mutants which produce CFTR proteins which are properly delivered to the plasma membrane but which are only residually or minimally active. Known mutants of CFTR are listed at http://www.genet.sickkids.on.ca/cftr-cgi-bin/fulltable. One can determine that a particular CFTR mutant is fully processed and reaches the plasma membrane in a Western blot assay using antibody against CFTR. Fully processed mutants achieve mature glycosylation status and appear on the gel as "band C and band B" whereas mutants that are retained in the endoplasmic reticulum are not fully glycosylated and show only "band B". See Example 2, below and Figure 1C.

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLES

Example 1: Deletion of a negatively charged region (a.a. 817-838) from the R domain of CFTR alters PKA-dependent regulation of the CFTR channel.

CFTR contains a large intracellular regulatory (R) domain where multiple PKA phosphorylation sites are located. There are two regions within the R domain that

contain a high proportion of negatively charged amino acids, a.a. 725-733 (NEG1) and a.a. 817-838 (NEG2). It is possible that these two regions could have allosteric or electrostatic interactions with other regions of CFTR and thus affect its chloride channel function. To test the role of NEG1 and NEG2, two deletion mutants, NEG1-CFTR and NEG2-CFTR, were created. The CFTR mutants were transiently expressed in HEK 293 cells, and their single channel functions were studied using the bilayer reconstitution system. Western blots indicate that both NEG1-CFTR and NEG2-CFTR process normally and traffic to the plasma membrane of HEK 293 cells. Both mutants form functional chloride channels in the bilayer membrane, with single channel conductances similar to the wt-CFTR channel. Like wt-CFTR, opening of NEG1-CFTR requires absolutely PKA phosphorylation and ATP binding/hydrolysis. In contrast to wt-CFTR, opening of NEG2-CFTR does not require PKA phosphorylation. Thus, deletion of NEG2, but not NEG1, alters PKA-dependent regulation of the CFTR chloride channel. Our data suggest that NEG2 could form a 'putative gating particle' of the CFTR channel possibly through electrostatic and/or allosteric interactions with other domains of CFTR.

Example 2: *Δ NEG1- and Δ NEG2-CFTR are glycosylated.*

The R domain of CFTR contains two negatively charged regions, amino acids 725-733 (NEG1) and amino acids 817-838 (NEG2), that reside in close proximity to two PKA phosphorylation sites, S737 and S813, used in vivo (Figure 1A) (Cheng, et al. 1991). NEG2 is predicted to form an amphipathic (-helical structure with a negatively charged face (Figure 1B) (Geourjon and Deleage, 1995, Rost and Sander, 1993, Rost and Sander, 1994). Three mutations (E822K, E826K, D836Y), two of

which were clearly obtained from patients with CF (E822K and D836Y), have been identified within the NEG2 region that result in the removal of negative charges (www.genet.sickkids.on.ca). The E822K CFTR channel has a low open probability relative to wt-CFTR (wild type-CFTR), but the E826K CFTR channel has single channel properties similar to wt-CFTR (Vankeerberghen et al., 1998). The presence of these disease-causing mutations suggests the potential importance of the NEG2 region. To investigate the roles of NEG1 and NEG2 in CFTR function, these regions were deleted from CFTR using mutagenesis and subcloning. The ΔNEG1- and ΔNEG2-CFTR proteins were transiently expressed in human embryonic kidney 293 cells. Membrane vesicles containing the CFTR proteins were isolated and subjected to SDS-PAGE. Like wt-CFTR, both ΔNEG1- and ΔNEG2-CFTR are present both in the core glycosylated (band B) and the fully glycosylated form (band C) (Figure 1C).

Example 3: *The open probability of the ΔNEG2-CFTR chloride channel is much less than that of wild type but is independent PKA, although it contains all PKA phosphorylation sites.*

Single channel measurements indicate that the ΔNEG1-CFTR channel is similar to wt-CFTR in its PKA dependence. No chloride channels are observed in the absence of PKA (Figure 2A) and the open probability in the presence of PKA and ATP is similar to wt-CFTR. In contrast, the ΔNEG2-CFTR channel opens without PKA (Figure 2A). The constitutive activity of the ΔNEG2-CFTR channel is unlikely to be due to the endogenous phosphorylation of the ΔNEG2-CFTR protein, since protein phosphatase 2A, which decreases activity of the wt-CFTR opened by PKA and ATP (Ma et al., 1997), has no effect on the ΔNEG2-CFTR channel (n=4). Moreover, addition of PKA up to 200 units/ml, four times the concentration required to fully

activate wt-CFTR (Ma et al., 1997), does not increase the open probability of the channel (Figure 2B). ΔNEG2-CFTR has conductance properties similar to wild type (Tao et al., 1996). However, the open probability of the ΔNEG2-CFTR chloride channel is much less than that of wild type and cannot be increased by PKA (P_o= 0.035 (0.012 and P_o= 0.026 (0.013 without and with PKA respectively, n=5). While NEG2 may represent an inhibitory region, removal of these amino acids does not result in a fully activated channel. The failure of the ΔNEG2-CFTR channel to respond to PKA does not result from inability of the channel to be phosphorylated, for an in vitro assay using (-^{32}P-ATP showed comparable phosphorylation of wt-CFTR and ΔNEG2-CFTR (Figure 1C). Thus, it appears that removal of NEG2 from CFTR completely eliminates the PKA dependence of the chloride channel, although the ΔNEG2-CFTR channel still contains all ten PKA sites and can be phosphorylated.

Example 4: *NEG2 polypeptide stimulates both wild-type and Δ NEG2 CFTR proteins at concentrations greater than 0.44 μM.*

To test whether the NEG2 region is responsible for both stimulatory and inhibitory interactions between the R domain and other domains, synthetic NEG2, a 22 amino acid peptide, was added to the cis-intracellular side of single CFTR channels captured in the planar lipid bilayer (Figure 3). The diary plot of open probability as a function of time shows the activity of a single wt-CFTR channel during the course of the experiment (Figure 3A). After peptide addition, there are periods of intense stimulation that last 4 to 8 minutes. These stimulatory periods are followed by either a return to the basal level of activity before peptide addition, or by an almost complete inhibition of the channel, where only a flickery 3 pS conductance is observed. During stimulation, the open probability more than doubles and more transitions are observed

between the open and closed states (Figure 3B). The stimulatory response was observed in 6 of 7 experiments at concentrations ≥0.44 μM (the remaining channel was inhibited upon peptide addition (4.4 μM) and no stimulation was seen). Profound inhibition was observed in three channels at concentrations ≥ 4.4 μM. When the NEG2 peptide was added to the intracellular side of the ΔNEG2-CFTR channel, which lacks its own endogenous NEG2 sequence, a similar stimulatory response was observed (Figure 3C).

Example 5: *The NEG2 peptide decreases the closed time of the wild-type CFTR protein.*

In order to understand the mechanism responsible for the increase in open probability, the gating kinetics of wt-CFTR without peptide and during stimulation by synthetic NEG2 were analyzed. The open time distributions of the wt-CFTR did not change during peptide stimulation, as both control (without NEG2 peptide) and peptide-stimulated channels had an open lifetime of approximately 120 ms (Figure 4A). Thus, the increase in the open probability is not due to a change in the closing rate of the channel. However, the closed time distribution for the stimulated channel is clearly shifted to the left compared to the control channel (Figure 4B). There are three components to the closed state, a fast (τ_{c1}), an intermediate (τ_{c2}), and a long (τ_{c3}) closed component. The fast closed component is probably due to closings within a burst (Carson et al., 1995). Therefore, to identify better the closed times between bursts, a delimiter of τ_c = 40 ms was set at the nadir between the fast and intermediate closed times (illustrated by the arrow in Figure 4B) to generate the closed-burst duration histograms. As shown in Figure 4C, following peptide stimulation, the intermediate closed time was reduced from 459 ms to 105 ms, whereas the long closed time

remained relatively unchanged. Thus, the interaction of NEG2 with CFTR increased the intermediate-opening rate of the channel. This increase in opening rate is similar to that observed when the phosphorylated R domain protein (amino acids 645-834) was added to CFTR- ΔR/S660A in excised, inside-out patches (Winter and Welsh, 1997). Additionally, modification of C832, which resides within NEG2, by N-ethylmaleimide (NEM) results in irreversible stimulation of PKA-phosphorylated CFTR chloride channel activity (Cotten and Welsh, 1997), further emphasizing the importance of NEG2 in CFTR regulation.

These data, taken together, show that the NEG2 region confers both stimulatory and inhibitory functions of the R domain on the CFTR channel. When this region is deleted from CFTR, the resultant channel opens without PKA (loss of inhibitory function), but it never achieves open probability comparable to wild type even when phosphorylated with PKA (loss of stimulatory function). This same sequence, expressed as a peptide, results in stimulation of channel openings at lower concentrations and profound inhibition of channel activity at higher concentrations, when added to the intracellular side of CFTR channels. It seems likely that this sequence interacts with CFTR at different sites on the nucleotide binding domains to either stimulate or inhibit channel openings. Phosphorylation of the R domain, in this model, changes its conformation and thus presents the NEG2 sequence better to the stimulatory than the inhibitory site. A current model for channel opening is that phosphorylated channels open in response to ATP binding and hydrolysis at the first nucleotide binding fold (NBF1) (Gadsby and Nairn, 1994, Ma and Davis, 1998). Since stimulation by NEG2 occurs by increasing channel openings, a likely site of stimulation is NBF1, though other models are possible.

METHODS USED IN EXAMPLES 1-5

Subcloning of CFTR gene

The wt, ΔNEG1-, and ΔNEG2-CFTR cDNAs were subcloned into an Epstein-Barr virus-based episomal eukaryotic expression vector, pCEP4 (Invitrogen, San Diego, CA), between the Nhe1 and Xho1 restriction sites. The ΔNEG1 and ΔNEG2 deletion mutants were created using the pALTER mutagenesis system and shuttled from pALTER into pCEP4 by substituting the corresponding fragment in pCEP4 wt-CFTR with the mutant fragment between the Xho1 and BstZ171 restriction sites. The ΔNEG1-CFTR cDNA has 27 bases deleted (amino acids 725-733). The ΔNEG2-CFTR cDNA has 66 bases deleted (amino acids 817-838).

Expression of CFTR in HEK 293 cells

A human embryonic kidney cell line (293-EBNA HEK; Invitrogen) was used for transfection and expression of the CFTR proteins (Ma et al., 1997, Ma et al., 1996, Xie et al., 1995). The HEK-293 cell line contains a pCMV-EBNA vector, which constitutively expresses the Epstein-Barr virus nuclear antigen-1 (EBNA-1) gene product and increases the transfection efficiency of Epstein-Barr virus-based vectors. The cells were maintained in Dulbecco's Modified Eagle Medium with 10% FBS and 1% L-glutamine. Geneticin (G418, 250 (g/ml) was added to the cell culture medium to maintain selection of the cells containing the pCMV-EBNA vector. Lipofectamine reagent (Life Technologies, Inc) in Optimem media (serum-free) was used to transfect the HEK-293 cells with pCEP4(wt), pCEP4(ΔNEG1), or pCEP4(ΔNEG2). After 5 hours, serum was added to the media (10% final serum concentration). Twenty-four hours after transfection, the transfection media was replaced with fresh media. The

cells were harvested two days after transfection and microsomal membrane vesicles were prepared for single channel measurements in the lipid bilayer reconstitution system.

Vesicle preparation from transfected HEK 293 cells

HEK-293 cells transfected with pCEP4(CFTR) were harvested and homogenized using a combination of hypotonic lysis and Dounce homogenization in the presence of protease inhibitors (Ma et al., 1997, Ma et al., 1996, Xie et al., 1995). Microsomes were collected by centrifugation of postnuclear supernatant (4500 x g, 15 min) at 100,000 x g for 20 min and resuspended in a buffer containing 250 mM sucrose, 10 mM HEPES, pH 7.2. The membrane vesicles were stored at -75°C until use.

In vitro phosphorylation of CFTR proteins

CFTR proteins isolated in membrane vesicles were bound to protein G agarose using a mouse monoclonal anti-human CFTR antibody (Genzyme). The protein G agarose was washed, and (-^{32}P-ATP (10 (Ci) and protein kinase A (~10 units/50(l) was added. Samples were incubated at 30(C for one hour during phosphorylation. Excess (γ-^{32}P-ATP was removed, and SDS-PAGE sample buffer (200 mM Tris-Cl, pH 6.7, 9% SDS, 6% beta-mercaptoethanol, 15% glycerol, and 0.01% bromophenol blue) was added to denature CFTR and release it from the protein G agarose. The samples were subjected to electrophoresis on a 5% SDS-polyacrylamide gel, transferred to a polyvinylidene difluoride membrane, and exposed to film.

Preparation of NEG2 peptides

The 22 amino acid peptide corresponding to NEG2 was custom made by Quality Controlled Biochemicals, Inc. The peptide was resuspended in water to a concentration of 1 mg/ml and pH was adjusted to a physiological range (7.2-7.4) using KOH and HCl. The space filling model of the NEG2 peptide was generated, based on secondary structure predictions (Geourjon and Deleage, 1995, Rost and Sander, 1993, Rost and Sander, 1994), using the Insight II program from Molecular Simulations Incorporated.

Reconstitution of CFTR channels in lipid bilayer membranes

Lipid bilayer membranes were formed across an aperture of ~200 (m diameter with a mixture of phosphatidylethanolamine:phosphatidylserine:cholesterol in a ratio of 5:5:1. The lipids were dissolved in decane at a concentration of 33 mg/ml. The recording solutions contained: cis (intracellular), 200 mM CsCl, 1 mM $MgCl_2$, 2 mM ATP, and 10 mM HEPES-Tris (pH 7.4); trans (extracellular), 50 mM CsCl, 10 mM HEPES-Tris (pH 7.4). Vesicles (1-4 (l) containing either wild-type, ΔNEG1-, or ΔNEG2-CFTR were added to the cis solution. The PKA catalytic subunit was present at a concentration of 50 units/ml in the cis solution unless noted otherwise. Single channel currents were recorded with an Axopatch 200A patch clamp unit (Axon Instruments). The currents were sampled at 1-2.5 ms/point. Single channel data analyses were performed with pClamp and TIPS softwares.

References

Anderson, M.P., Berger, H.A., Rich, D.P., Gregory, R.J., Smith, A.E., and Welsh, M.J. (1991). Nucleoside triphosphates are required to open the CFTR chloride channel. Cell

67, 775-784.

Bear, C.E., Li, C., Kartner, N., Bridges, R.J., Jensen, T.J., Ramjeesingh, M., and Riordan, J.R. (1992). Purification and functional reconstitution of the cystic fibrosis transmembrane conductance regulator (CFTR). Cell 68, 809-818.

Carson, M.R., Travis, S.M., and Welsh, M.J. (1995). The two nucleotide-binding domains of cystic fibrosis transmembrane conductance regulator (CFTR) have distinct functions in controlling channel activity. J. Biol. Chem. 270, 1711-1717.

Cheng, S.H., Rich, D.P., Marshall, J., Gregory, R.J., Welsh, M.J., and Smith, A.E. (1991). Phosphorylation of the R domain by cAMP-dependent protein kinase regulates the CFTR chloride channel. Cell 66, 1027-1036.

Cotten, J.F. and Welsh, M.J. (1997). Covalent modification of the regulatory domain irreversibly stimulates cystic fibrosis transmembrane conductance regulator. J. Biol. Chem. 272, 25617-25622.

Dulhanty, A.M. and Riordan, J.R. (1994). Phosphorylation by cAMP-dependent protein kinase causes a conformational change in the R domain of the cystic fibrosis transmembrane conductance regulator. Biochemistry 22, 4072-4079.

Gadsby, D.C. and Nairn, A.C. (1994). Regulation of CFTR channel gating. Trends Biochem. Sci. 19, 513-518.

Geourjon, C. and Deleage, G. (1995). SOPMA: significant improvements in protein secondary structure prediction by consensus prediction from multiple alignments. CABIOS 11, 681-684.

Gunderson, K.L. and Kopito, R.R. (1995). Conformational states of CFTR associated with channel gating: the role of ATP binding and hydrolysis. Cell 82, 231-239.

Higgens, C.F. (1992). ABC transporters: from microorganisms to man. Annu. Rev. Cell

Biol. 8, 67-113.

Ma, J. and Davis, P.B. (1998). What we know and what we do not know about cystic fibrosis transmembrane conductance regulator. Clinics in Chest Medicine 19, 459-471.

Ma, J., Tasch, J.E., Tao, T., Zhao, J., Xie, J., Drumm, M.L., and Davis, P.B. (1996). Phosphorylation-dependent block of cystic fibrosis transmembrane conductance regulator chloride channel by exogenous R domain protein. J. Biol. Chem. 271, 7351-7356.

Ma, J., Zhao, J., Drumm, M.L., Xie, J., and Davis, P.B. (1997). Function of the R domain in the cystic fibrosis transmembrane conductance regulator chloride channel. J. Biol. Chem. 272, 28133-28141.

Picciotto, M.R., Cohn, J.A., Bertuzzi, G., Greengard, P., and Nairn, A.C. (1992). Phosphorylation of the cystic fibrosis transmembrane conductance regulator. J. Biol. Chem. 267, 12742-12752.

Quinton, P.M. (1986). Missing Cl^- conductance in cystic fibrosis. Am. J. Physiol. 251, C649-C652.

Rich, D.P., Berger, H.A., Cheng, S.H., Travis, S.M., Saxena, M., Smith, A.E., and Welsh, M.J. (1993). Regulation of the cystic fibrosis transmembrane conductance regulator Cl^- channel by negative charge in the R domain. J. Biol. Chem. 268, 20259-20267.

Rich, D.P., Gregory, R.J., Anderson, M.P., Manavalan, P., Smith, A.E., and Welsh, M.J. (1991). Effect of deleting the R domain on CFTR-generated chloride channels. Science 253, 205-207.

Riordan, J., Rommens, J., Kerem, B.-S., Noa, A., Rozmahel, R., Grzelczak, Z., Zielenski, J., Lok, S., Plavsic, N., Chou, J.-L., Drumm, M., Iannuzzi, M., Collins, F.,

and Tsui, L.-C. (1989). Identification of the cystic fibrosis gene: cloning and characterization of complementary DNA. Science 245, 1066-1073.

Rost, B. and Sander, C. (1993). Prediction of protein structure at better than 70% accuracy. J. Mol. Biol. 232, 584-599.

Rost, B. and Sander, C. (1994). Combining evolutionary information and neural networks to predict protein secondary structure. Proteins 19, 55-72.

Tabcharani, J.A., Chang, X.-B., Riordan, J.R. and Hanrahan, J.W. (1991). Phosphorylation-regulated Cl- channel in CHO cells stably expressing the cystic fibrosis gene. Nature 352, 628-631.

Tao, T., Xie, J., Drumm, M.L., Zhao, J., Davis, P.B., and Ma, J. (1996). Slow conversions among subconductance states of cystic fibrosis transmembrane conductance regulator chloride channel. Biophys. J. 70, 743-753.

Vankeerberghen, A., Wei, L., Jaspers, M., Cassiman, J.-J., Nilius, B., and Cuppens, H. (1998). Characterization of 19 disease-associated missense mutations in the regulatory domain of the cystic fibrosis transmembrane conductance regulator. Hum. Mol. Genet. 7, 1761-1769.

Welsh, M.J. and Smith, A.E. (1993). Molecular mechanisms of CFTR chloride channel dysfunction in cystic fibrosis. Cell 73, 1251-1254.

Winter, M.C. and Welsh, M.J. (1997). Stimulation of CFTR activity by its phosphorylated R domain. Nature 389, 294-296.

Xie, J., Drumm, M.L., Ma, J., and Davis, P.B. (1995). Intracellular loop between transmembrane segments IV and V of cystic fibrosis transmembrane conductance regulator is involved in regulation of chloride channel conductance state. J. Biol. Chem. 270, 28084-28091.

Zielenski, J. and Tsui, L.C. (1995). Cystic fibrosis: genotypic and phenotypic variations. Annu. Rev. Genetics 29, 777-807.

CLAIMS:

1. An isolated polypeptide comprising a portion of CFTR (cystic fibrosis transmembrane conductance regulator) protein of between 10 and 100 amino acids, said portion comprising 18 amino acids as shown in SEQ ID NO: 1.

2. The polypeptide of claim 1 which comprises 22 amino acids as shown in SEQ ID NO: 2.

3. The polypeptide of claim 1 wherein the polypeptide is fused to a membrane-penetrating peptide.

4. The polypeptide of claim 2 wherein the polypeptide is fused to a membrane-penetrating peptide.

5. The polypeptide of claim 3 wherein the membrane-penetrating peptide is selected from the group consisting of: VP-22 (SEQ ID NO: 3), (SEQ ID NO: 4), and (SEQ ID NO: 5).

6. The polypeptide of claim 4 wherein the membrane-penetrating peptide is selected from the group consisting of: VP-22 (SEQ ID NO: 3), (SEQ ID NO: 4), and (SEQ ID NO: 5).

7. The polypeptide of claim 1 which is free of phosphorylation.

8. A method of activating a CFTR protein comprising:

applying a polypeptide to a CFTR protein which forms a cAMP regulated chloride channel, said polypeptide comprising a portion of CFTR protein of between about 10 and 100 amino acids, said portion comprising 18 amino acids as shown in SEQ ID NO: 1, whereby the open probability of the channel formed by the CFTR increases by at least 25%.

9. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 50%.

10. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 75%.

11. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 100%.

12. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 125%.

13. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 150%.

14. The method of claim 8 wherein the open probability of the channel formed by the CFTR increases by at least 200%.

15. The method of claim 8 wherein the CFTR protein is a mutant which reaches a cell's plasma membrane but fails to undergo full activation.

16. The method of claim 15 wherein the CFTR protein is listed at http://www.genet.sickkids.on.ca/cftr-cgi-bin/fulltable.

17. The method of claim 8 wherein the step of applying is performed by administering an aerosolized polypeptide to a patient with a mutant CFTR protein.

18. The method of claim 8 wherein the CFTR protein is in a lipid bilayer and a change in conductance is measured upon applying the polypeptide.

19. The method of claim 8 wherein the step of applying the polypeptide is accomplished by administering a nucleic acid encoding the polypeptide to a patient who expresses the CFTR protein, whereby the polypeptide is

expressed.

20. The method of claim 19 wherein the nucleic acid is administered as an aerosol to the patient's airways.

21. A method of activating a CFTR protein comprising:

applying a polypeptide to a CFTR protein which forms a cAMP regulated chloride channel, said polypeptide comprising a portion of CFTR protein of between 10 and 100 amino acids, said portion comprising 22 amino acids as shown in SEQ ID NO: 1, whereby the open probability of the channel formed by the CFTR increases by at least 25%.

22. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 50%.

23. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 75%.

24. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 100%.

25. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 125%.

26. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 150%.

27. The method of claim 21 wherein the open probability of the channel formed by the CFTR increases by at least 200%.

28. The method of claim 21 wherein the CFTR protein is a mutant which reaches a cell's plasma membrane but fails to undergo full activation.

29. The method of claim 28 wherein the CFTR protein is listed at http://www.genet.sickkids.on.ca/cftr-cgi-bin/fulltable.

30. The method of claim 21 wherein the step of applying is performed by administering an aerosolized polypeptide to a patient with a mutant CFTR protein.

31. The method of claim 21 wherein the CFTR protein is in a lipid bilayer and a change in conductance is measured upon applying the polypeptide.

32. The method of claim 21 wherein the step of applying the polypeptide is accomplished by administering a nucleic acid encoding the polypeptide to a patient who expresses the CFTR protein, whereby the polypeptide is expressed.

33. The method of claim 32 wherein the nucleic acid is administered as an aerosol to the patient's airways.

34. The method of claim 8 or 21 wherein the polypeptide is free of phosphorylation.

ENHANCERS OF CFTR CHLORIDE CHANNEL FUNCTION

ABSTRACT

Phosphorylation of the cystic fibrosis transmembrane conductance regulator (CFTR) by cyclic AMP-dependent protein kinase (PKA) is essential for opening the CFTR chloride channel. A short segment containing many negatively charged amino acids (817-838, NEG2) within the regulatory (R) domain of CFTR is a critical regulator of the chloride channel activity. Deletion of NEG2 from CFTR completely eliminates the PKA dependence of the chloride channel. Exogenous NEG2 peptide interacts with the CFTR molecule and exhibits stimulatory effects on CFTR function. Our data suggest that NEG2 interacts with other cytosolic domains of CFTR to control the opening transitions of the chloride channel.

SEQUENCE LISTING

SEQ ID NO: 1 GLEISEEINEEDLKECFF

SEQ ID NO: 2 GLEISEEINEEDLKECFFDDME

SEQ ID NO: 3 VP-22 (Phelan et al., Nature Biotech 16:440-443, 1998, incorporated by reference herein)

SEQ ID NO: 4 GWTLNSAGYLLGKINLKALAALAKKIL (amide)

SEQ ID NO: 5 RQIKIWFQNRRMKWKK (amide)

Fig. 1

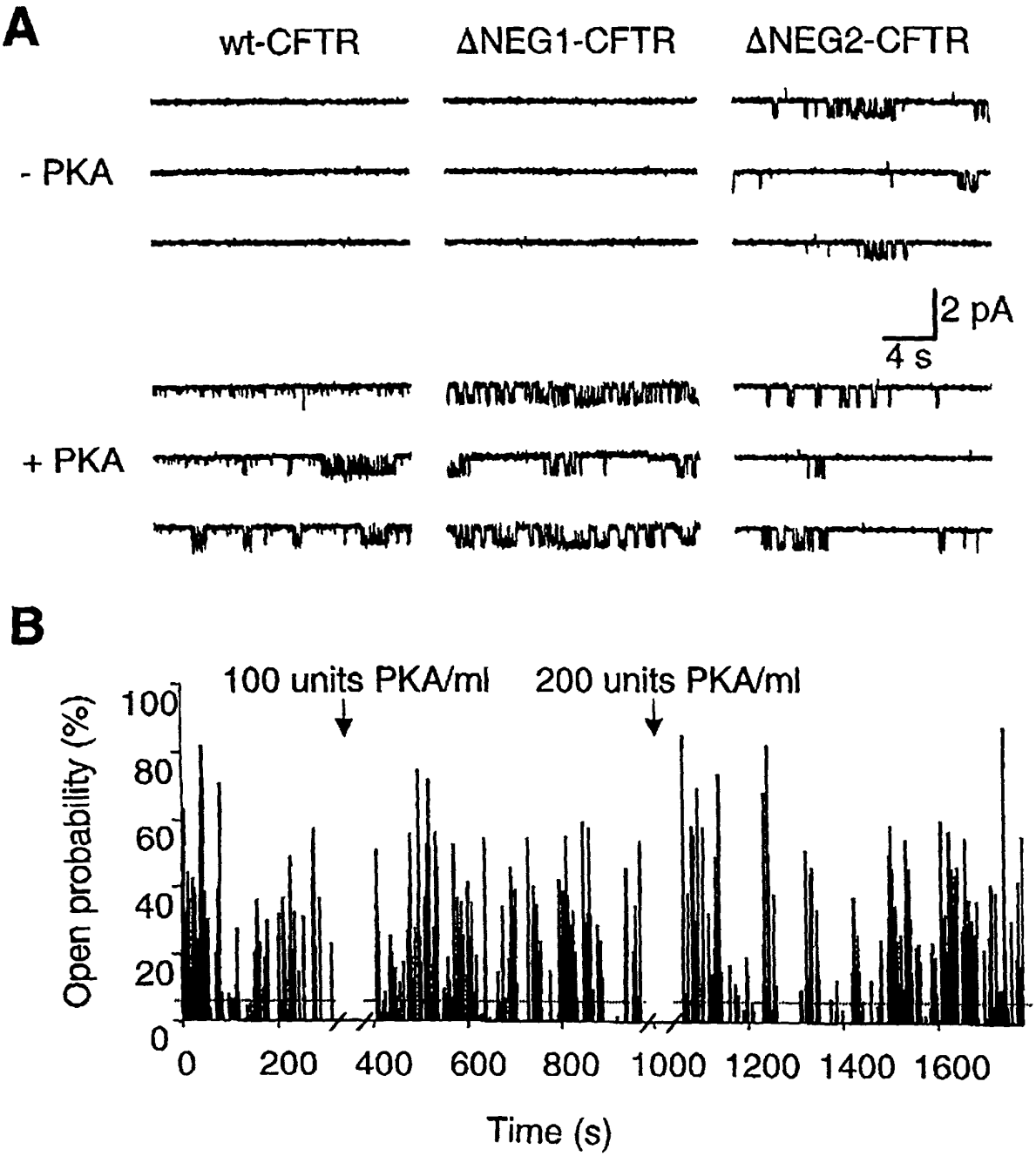

A
wt-CFTR
ΔNEG1-CFTR
ΔNEG2-CFTR
- PKA
+ PKA
2 pA
4 s
B
100 units PKA/ml
200 units PKA/ml
Open probability (%)
100
80
60
40
20
0
0
200
400
600
800
1000
1200
1400
1600
Time (s)

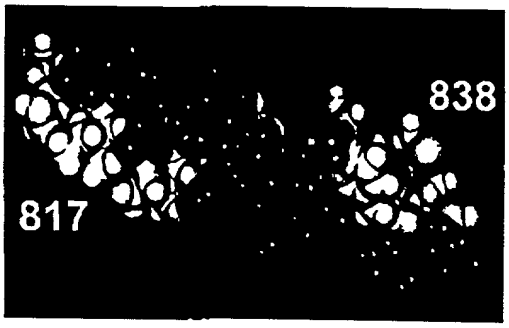
Fig. 2

A

NEG1 725 E E D S D E P L E 733

NEG2 817 G L E I S E E I N E E D L K E C F F D D M E 838

B



C

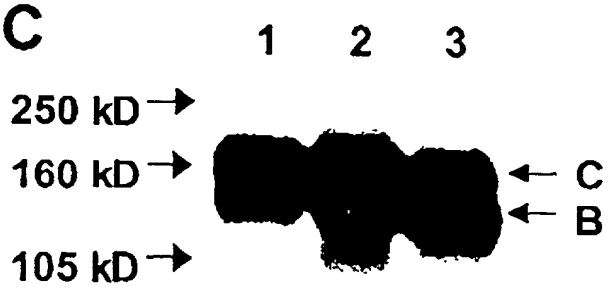


Fig. 3

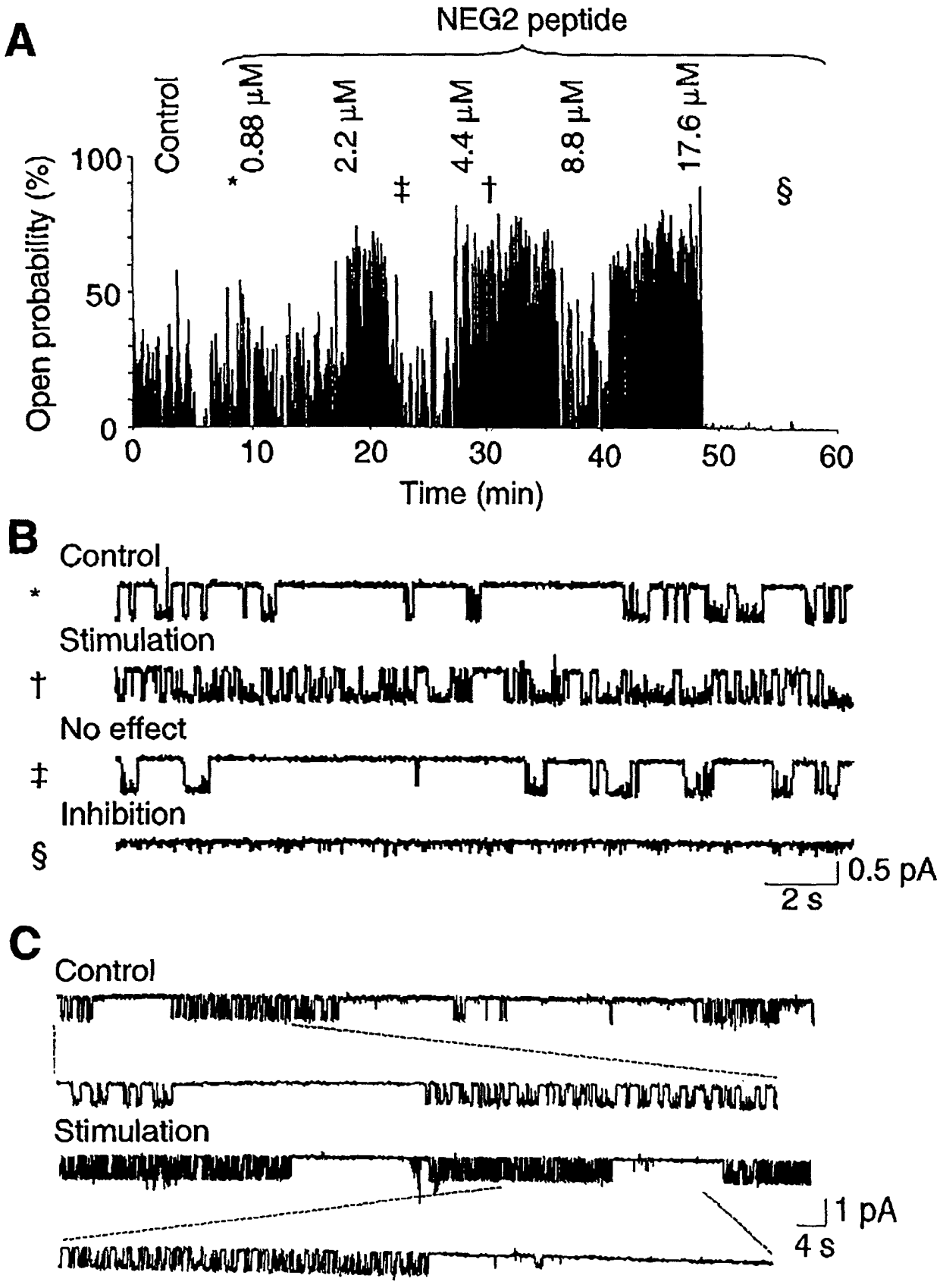
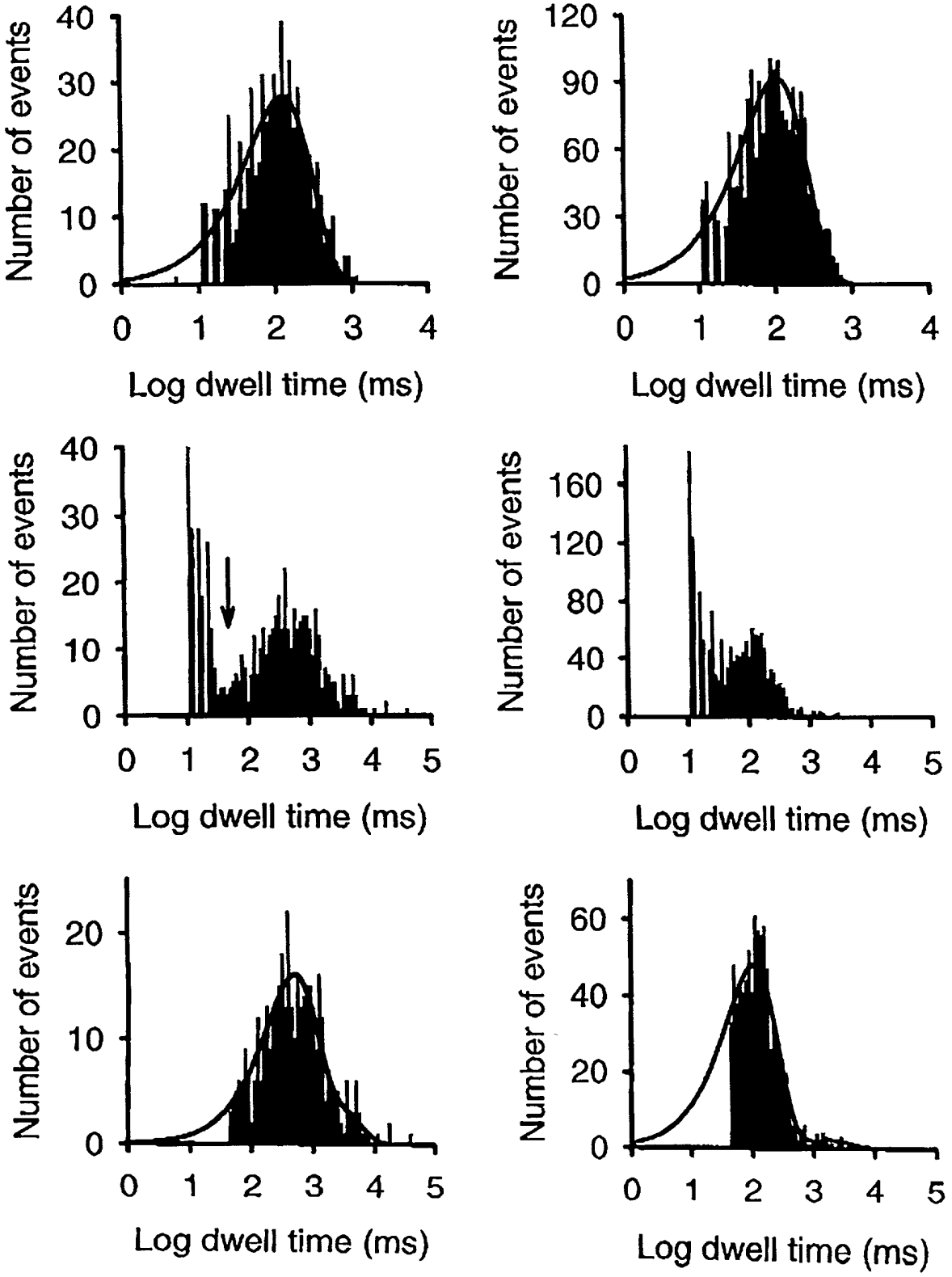

A
NEG2 peptide
Control
0.88 µM
2.2 µM
4.4 µM
8.8 µM
17.6 µM
*
‡
†
§
Open probability (%)
100
50
0
0
10
20
30
40
50
60
Time (min)
B
Control
*
Stimulation
†
No effect
‡
Inhibition
§
0.5 pA
2 s
C
Control
Stimulation
1 pA
4 s

Fig. 4


Number of events
Log dwell time (ms)
0
10
20
30
40
90
60
120
80
160
1
2
3
4
5